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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/848,852ADATE: 12/20/2001
TIME: 11:52:09Input Set : N:\Crf3\RULE60\09848852.raw
Output Set: N:\CRF3\12202001\I848852A.rawRECEIVED
JAN 18 2002
TECH CENTER 1600/2900SEQUENCE LISTING
ENTERED

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hillman, Jennifer L.
Tang, Y. Tom
Corley, Neil C.
Guegler, Karl J.
Yue, Henry
Patterson, Chandra

(ii) TITLE OF INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US/09/848,852A
(B) FILING DATE: 07-May-2001

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/069,725
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0515 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
(B) CLONE: 1281694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Asn Asp Ser Leu Arg Thr Asp Val Phe Val Arg Phe Gln Pro Glu

64 1

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66	Ser Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Thr Leu Glu Ile			
67	20	25	30	
68	Pro Leu Pro Asn Arg Pro His Trp Phe Leu Leu Phe Gly Ala Thr Glu			
69	35	40	45	
70	Glu Glu Ile Gln Glu Ile Cys Leu Lys Ile Leu Gln Leu Tyr Ala Arg			
71	50	55	60	
72	Lys Lys Val Asp Leu Thr His Leu Glu Gly Glu Val Glu Lys Arg Lys			
73	65	70	75	80
74	His Ala Ile Glu Glu Ala Lys Ala Gln Ala Arg Gly Leu Leu Pro Gly			
75	85	90	95	
76	Gly Thr Gln Val Leu Asp Gly Thr Ser Gly Phe Ser Pro Ala Pro Lys			
77	100	105	110	
78	Leu Val Glu Ser Pro Lys Glu Gly Lys Gly Ser Lys Pro Ser Pro Leu			
79	115	120	125	
80	Ser Val Lys Asn Thr Lys Arg Arg Leu Glu Gly Ala Lys Lys Ala Lys			
81	130	135	140	
82	Ala Asp Ser Pro Val Asn Gly Leu Pro Lys Gly Arg Glu Ser Arg Ser			
83	145	150	155	160
84	Arg Ser Arg Ser Arg Glu Gln Ser Tyr Ser Arg Ser Pro Ser Arg Ser			
85	165	170	175	
86	Ala Ser Pro Lys Arg Arg Lys Ser Asp Ser Gly Ser Thr Ser Gly Gly			
87	180	185	190	
88	Ser Lys Ser Gln Ser Arg Ser Arg Ser Arg Ser Asp Ser Pro Pro Arg			
89	195	200	205	
90	Gln Ala Pro Arg Ser Ala Pro Tyr Lys Gly Ser Glu Ile Arg Gly Ser			
91	210	215	220	
92	Arg Lys Ser Lys Asp Cys Lys Tyr Pro Gln Lys Pro His Lys Ser Arg			
93	225	230	235	240
94	Ser Arg Ser Ser Arg Ser Arg Ser Arg Ser Arg Glu Arg Ala Asp			
95	245	250	255	
96	Asn Pro Gly Lys Tyr Lys Lys Ser His Tyr Tyr Arg Asp Gln Arg			
97	260	265	270	
98	Arg Glu Arg Ser Arg Ser Tyr Glu Arg Thr Gly Arg Arg Tyr Glu Arg			
99	275	280	285	
100	Asp His Pro Gly His Ser Arg His Arg Arg			
101	290	295		
103	(2) INFORMATION FOR SEQ ID NO: 2:			
105	(i) SEQUENCE CHARACTERISTICS:			
106	(A) LENGTH: 3464 base pairs			
107	(B) TYPE: nucleic acid			
108	(C) STRANDEDNESS: single			
109	(D) TOPOLOGY: linear			
111	(vii) IMMEDIATE SOURCE:			
112	(A) LIBRARY: COLNNOT16			
113	(B) CLONE: 1281694			
115	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
117	TTCGTGAAGC ACTCCATGG A GCATGTGTCA ATGGCCTGTG TCCACCTGGC TTCCAAGATA	60		
118	GAAGAGGCC CAAGACGCAT ACGGGACGTC ATCAATGTGT TTCACCGCCT TCGACAGCTG	120		
119	AGAGACAAAA AATAATCGTT ATGTACCTTC AGGTGTTAGA GTGTGAGCGT AACCAACACC	180		

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120	TGGTCCAGAC	CTCATGGGTA	GCCTCTGAGG	GTAAGTGACT	AAGACTTCTC	CTCTGCTGTC	240	
121	CAAGCGCTT	GGTGCAGGGA	CAGCGGCATC	TTCAGCCAAT	CCAGTGCAGG	CTCTCCACCG	300	
122	AAGGCTGGCT	CTAGACTGGT	GACCCCTGT	TGAAATGGGA	CAGTTGGCAG	CGGCTCTGAT	360	
123	GAGCCCGAGA	AGAGGCCTGC	CCTTGGGTGC	GGAGTCTCCC	TCCGCACGAT	GCTCCCACGC	420	
124	GTCCAACTTG	CACCCAAGGG	GCTTTCCCT	CTTCCAAGTG	GACTCCTCA	AGGAAGCTGC	480	
125	AGCTCGGTCA	GCAGAGAAGG	GGCCTGCCGC	CAGCGCCCTG	GAGGAAGAGG	AAGAGGAACC	540	
126	CAAGAGGATG	GCTTGTCTCC	CAGCAGCCAC	ACCGGCTTTG	TGCTCAGCCA	GTTCATTGTA	600	
127	GTTTGCATGT	TTCTCTGCAC	TATGGATTT	GAGCATTAG	ATTTCTTAA	TCAAAAGCGT	660	
128	TTTAGTGA	CCAGTAGACA	TTTTCTTCT	GAGGCATCGT	GCTTTGCATG	AGAGCAGGCC	720	
129	AAGGTTGAGG	GGAAAAGTAA	AGTTAAAGTC	GGTCTCTTT	CATAGCAACA	CGTATTGTCT	780	
130	GACATTCA	CAGCTTTTT	TTTTTCTAA	AATTCTGTG	CCTTCTGTC	CTGTATTAC	840	
131	TGTATTTAGA	AAAAGCAGCT	AGAATATTC	TCCATTA	ACT	CTTGAGATT	ACAGGACTGT	900
132	CTAGCTCTGA	GTCCTAGCAA	TAGACTCCTT	AGAGGAGTAG	TACGTTTATC	TAGATTTCT	960	
133	CTAGATAATG	CAGGCGGAAG	ACCTGGGTT	CCGGGTGGGG	CATTGCAGTT	CTTCCTGTGT	1020	
134	TTGGCTTCCA	GGAAATTACAT	GAACGACAGC	CTTCGCACCG	ACGTCTCGT	GCGGTTCCAG	1080	
135	CCAGAGAGCA	TCGCCTGTGC	CTGCATTAT	CTTGCTGCC	GGACGCTGGA	GATCCCTTTG	1140	
136	CCCAATCGTC	CCCATTGGTT	TCTTTGTTT	GGAGCAACTG	AAGAAGAAAT	TCAGGAAATC	1200	
137	TGCTTAAAGA	TCTTGCAGCT	TTATGCTCGG	AAAAAGGTTG	ATCTCACACA	CCTGGAGGGT	1260	
138	GAAGTGGAAA	AAAGAAAGCA	CGCTATCGAA	GAGGCAAAGG	CCCAAGCCG	GGGCCTGTTG	1320	
139	CCTGGGGGCA	CACAGGTGCT	GGATGGTACC	TCGGGGTTCT	CTCCTGCC	CAAGCTGGT	1380	
140	GAATCCCCA	AAGAAGGTAA	AGGGAGCAAG	CCTCCCCAC	TGTCTGTGAA	GAACACCAAG	1440	
141	AGGAGGCTGG	AGGGCGCCAA	GAAAGCCAAG	GC GGACAGCC	CCGTGAACGG	CTTGCCAAAG	1500	
142	GGGCGAGAGA	GTCGGAGTCG	GAGCCGGAGC	CGTGAGCAGA	GCTACTCGAG	GTCCCCATCC	1560	
143	CGATCAGCGT	CTCCTAACAGAG	GAGGAAAAGT	GACAGCGGCT	CCACATCTGG	TGGGTCCAAG	1620	
144	TCGCAGAGCC	GCTCCCGGAG	CAGGAGTGC	TCCCCACCGA	GACAGGGCCC	CCGCAGCGCT	1680	
145	CCCTACAAAG	GCTCTGAGAT	TCGGGGCTCC	CGGAAGTCCA	AGGACTGCAA	GTACCCCCAG	1740	
146	AAGCCACACA	AGTCTCGGAG	CCGGAGTCT	TCCCGTTCTC	GAAGCAGGTC	ACGGGAGCGG	1800	
147	GCGGATAATC	CGGGAAAATA	CAAGAAGAAA	AGTCATTACT	ACAGAGATCA	GCGACGAGAG	1860	
148	CGCTCGAGGT	CGTATGAACG	CACAGGCCGT	CGCTATGAGC	GGGACCACCC	TGGGCACAGC	1920	
149	AGGCATCGGA	GGTGAGGCCG	GGTTGCAGTG	ACTGGTGGCC	GCAAGCCCTT	CCCTGGGGAG	1980	
150	TACCTGATGG	CTGCCCTTTG	ACCCCCGGT	GCTGCCCTT	GACCCCGGG	TGTGCTCTCA	2040	
151	GCGCAAGTGG	TCCTAGAAC	GGATTCTTT	TGAAATGTC	TGTCGACTGG	ACCTTGGTGG	2100	
152	ATTGGAAAT	GGAACTGAGG	GACCGGTGAC	ACGTGCTTC	GACCGGTCTG	GGGTGCGGCG	2160	
153	CACACCTGGG	CCCCTGCAGG	GCTCAGCTCG	GCAGCAGCTC	TGAGGGCAGC	TCAATGAAA	2220	
154	AGTGAATGCA	CACGCCCTG	TTGGCGTGGC	CTGGCATGGC	CTGGTGTAT	CGGCAGCCGC	2280	
155	TCTCCACTCC	CCGACTGATA	CTCAATTACG	TGAAGCCAAG	AAAGATGATT	TTTGAACCT	2340	
156	TTGCCTATAT	TAGGTTGTAC	TTATGTACAT	ATTTGCA	GTTTCACAGG	AGAAAGTGGC	2400	
157	CTTAAC	TGCCCTTCTC	TCTCCACGTT	GTAAATAAAC	ATGTGTTAA	TACAAGTTAA	2460	
158	AGCTATGTAT	GAAAAC	TCAGCT	AACTTGAATC	CCGTCA	AAAAC	2520	
159	TGACTTTAA	AATGTGAGGG	TATTTGGATC	TGTGTTGAAA	GTCGTAT	TTTATCTGTG	2580	
160	CGGTGCTGAG	TGCAGGCCAC	CAGCTCTAA	ATAGAGGTT	CCTATATGCG	CGTATGACAT	2640	
161	GGTGAATAAA	CACAACTCTC	TCCACTCAGG	ACATCCGGAG	CGTTATGGAC	GTGGTAGGTG	2700	
162	GTCGTTCTGT	GTGCTTGTGA	AAGTGTCCAG	GCGTGTGCAC	AGCCAGTGCG	CCCACTTCCG	2760	
163	GGCTCCTTGC	TCCCTGCTGT	ACTGAAGTT	TGGATTTGC	ATCCAATCCT	GTGTGCCTGC	2820	
164	CCTTCTGCCG	AAGCTTGTGA	GGGGCCTGAG	TCCCTGCC	ATCAGGATGA	CAGGCTCCTT	2880	
165	CCTGCAGGGC	CATAGGAGGG	AAGTTTTGGA	AACACAGAA	GATTCCAAGG	TGCTCTCGTT	2940	
166	CCTGAGGGGG	ACTGTTTGT	AACCCATGAC	ATCTGTGGC	GAGAGAGGCA	GCTGGGAGCA	3000	
167	GGACACTTGG	AGGGTCACCC	CACGGGGTG	GCACCTGCAC	TCTGAGTGC	CCCCACTGTC	3060	
168	ATCAGCTGCC	TCTTACCGTG	GACACAGTT	TGGTTTGGG	GACTAGGGGG	CCCCACTCCT	3120	

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169	GGTGGTACCG TTTGGACTTA CTAGGGCAGT GGGACATATA GGCGGGGCT AGTGGGATAA	3180
170	CGGGGAGTTA CGCCTGATGA CTTTTTGAT GGAATCCTGC ATTAGATAGC TGGTGGGACC	3240
171	CCCCCCTCAG AATTGGGAA CTGAGGAGAC TCCAGGGAGG GTGTCTTCC AGGGAGAGCA	3300
172	GCTATGAGGG GCCCCCCTAGC TTCCTGTGCC TGGAAAGTAAG AGAACCAAGTA AAGGGCCATA	3360
173	CACACCTGTA CCCAAGAGAC CGCTCTCCAT TTGCTTTCTT TTTTTACTAA ATAATTGTAA	3420
174	AATATTATTA TGACATAAAG ACCATTAA GGCCAAAAAA AAAA	3464

176 (2) INFORMATION FOR SEQ ID NO: 3:

178 (i) SEQUENCE CHARACTERISTICS:
 179 (A) LENGTH: 332 amino acids
 180 (B) TYPE: amino acid
 181 (C) STRANDEDNESS: single
 182 (D) TOPOLOGY: linear

184 (vii) IMMEDIATE SOURCE:

185 (A) LIBRARY: BEPINOT01
 186 (B) CLONE: 2056178

188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

190	Met Tyr Ser Ala Gln Arg Phe Trp Gly Thr Ile Trp Ala Arg Arg Gly	
191	1 5 10 15	
192	Ala His Leu Ala Pro Pro Asp Ala Ser Ile Leu Ile Ser Asn Val Cys	
193	20 25 30	
194	Ser Ile Gly Asp His Val Ala Gln Glu Leu Phe Gln Gly Ser Asp Leu	
195	35 40 45	
196	Gly Met Ala Glu Glu Ala Glu Arg Pro Gly Glu Lys Ala Gly Gln His	
197	50 55 60	
198	Ser Pro Leu Arg Glu Glu His Val Thr Cys Val Gln Ser Ile Leu Asp	
199	65 70 75 80	
200	Glu Phe Leu Gln Thr Tyr Gly Ser Leu Ile Pro Leu Ser Thr Asp Glu	
201	85 90 95	
202	Val Val Glu Lys Leu Glu Asp Ile Phe Gln Gln Glu Phe Ser Thr Pro	
203	100 105 110	
204	Ser Arg Lys Gly Leu Val Leu Gln Leu Ile Gln Ser Tyr Gln Arg Met	
205	115 120 125	
206	Pro Gly Asn Ala Met Val Arg Gly Phe Arg Val Ala Tyr Lys Arg His	
207	130 135 140	
208	Val Leu Thr Met Asp Asp Leu Gly Thr Leu Tyr Gly Gln Asn Trp Leu	
209	145 150 155 160	
210	Asn Asp Gln Val Met Asn Met Tyr Gly Asp Leu Val Met Asp Thr Val	
211	165 170 175	
212	Pro Glu Lys Val His Phe Phe Asn Ser Phe Phe Tyr Asp Lys Leu Arg	
213	180 185 190	
214	Thr Lys Gly Tyr Asp Gly Val Lys Arg Trp Thr Lys Asn Val Asp Ile	
215	195 200 205	
216	Phe Asn Lys Glu Leu Leu Ile Pro Ile His Leu Glu Val His Trp	
217	210 215 220	
218	Ser Leu Ile Ser Val Asp Val Arg Arg Arg Thr Ile Thr Tyr Phe Asp	
219	225 230 235 240	
220	Ser Gln Arg Thr Leu Asn Arg Arg Cys Pro Lys His Ile Ala Lys Tyr	
221	245 250 255	
222	Leu Gln Ala Glu Ala Val Lys Lys Asp Arg Leu Asp Phe His Gln Gly	

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223	260	265	270
224	Trp Lys Gly Tyr Phe Lys Met Asn Val Ala Arg Gln Asn Asn Asp Ser		
225	275	280	285
226	Asp Cys Gly Ala Phe Val Leu Gln Tyr Cys Lys His Leu Ala Leu Ser		
227	290	295	300
228	Gln Pro Phe Ser Phe Thr Gln Gln Asp Met Pro Lys Leu Arg Arg Gln		
229	305	310	315
230	Ile Tyr Lys Glu Leu Cys His Cys Lys Leu Thr Val		
231	325	330	

233 (2) INFORMATION FOR SEQ ID NO: 4:

235 (i) SEQUENCE CHARACTERISTICS:
 236 (A) LENGTH: 1991 base pairs
 237 (B) TYPE: nucleic acid
 238 (C) STRANDEDNESS: single
 239 (D) TOPOLOGY: linear

241 (vii) IMMEDIATE SOURCE:

242 (A) LIBRARY: BEPINOT01
 243 (B) CLONE: 2056178

245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

247	GCCTCCCTGT	CCCCGACCC	TCTTTGATG	CCTCAGCAAG	TGAAGAGGAG	GAAGAAAGAGG	60
248	AGGAGGAGGA	GGATGAAGAT	GAAGAGGAGG	AAGTGGCAGC	TTGGAGGCTG	CCCCCAAGAT	120
249	GGAGTCAGCT	GGGAACCTCC	CAGCGGCC	GCCCTTCCC	CCCCACTCAT	CGAAAAAACCT	180
250	GCTCACAGCG	CCGCGGCCGA	GCCATGAGAG	CCTTCCGGAT	GCTGCTCTAC	TCAAAAAGCA	240
251	CCTCGCTGAC	ATTCCACTGG	AAGCTTGGG	GGGCCACCG	GGGCCGGCGG	CGGGGCCTCG	300
252	CACACCCAA	GAACCATCTT	TCACCCCAGC	AAGGGGTGC	GACGCCACAG	GTGCCATCCC	360
253	CCTGTTGTCG	TTTGACTCC	CCCCGGGGC	CACTTCCACC	CCGGCTGGGT	CTGCTAGGTG	420
254	CTCTCATGGC	TGAGGATGGG	GTGAGAGGGT	CTCCACCACT	GCCCTCTGGG	CCCCCATGG	480
255	AGGAAGATGG	ACTCAGGTGG	ACTCCAAAGT	CTCCCTCTGGA	CCCTGACTCG	GGCCTCCTT	540
256	CATGTACTCT	GCCCAACGGT	TTTGGGGAC	AATCTGGGCC	AGAAGGGAG	CGCACTTGGC	600
257	ACCCCTGAT	GCCAGCATCC	TCATCAGCA	TGTGTGCAGC	ATCGGGGACC	ATGTGGCCA	660
258	GGAGCTTTT	CAGGGCTCAG	ATTGGGCAT	GGCAGAAAGAG	GCAGAGAGGC	CTGGGGAGAA	720
259	AGCCGGCCAG	CACAGCCCC	TGCGAGAGGA	GCATGTGACC	TGCGTACAGA	GCATCTTGG	780
260	CGAATTCTT	CAAACGTATG	GCAGCCTCAT	ACCCCTCAGC	ACTGATGAGG	TAGTAGAGAA	840
261	GCTGGAGGAC	ATTTCAGC	AGGAGTTTC	CACCCCTTC	AGGAAGGGCC	TGGTGTGCA	900
262	GCTGATCCAG	TCTTACCAAGC	GGATGCCAGG	CAATGCCATG	GTGAGGGCT	TCCGAGTGGC	960
263	TTATAAGCGG	CACGTGCTGA	CCATGGATGA	CTTGGGGACC	TTGTATGGAC	AGAACTGGCT	1020
264	CAATGACCAAG	GTGATGAACA	TGTATGGAGA	CCTGGTCATG	GACACAGTCC	CTGAAAAGGT	1080
265	GCATTCTTC	AATAGTTCT	TCTATGATAA	ACTCCGTACC	AAGGGTTATG	ATGGGGTGAA	1140
266	AAGGTGGACC	AAAAACGTGG	ACATCTCAA	TAAGGAGCTA	CTGCTAATCC	CCATCCACCT	1200
267	GGAGGTGCAT	TGGTCCCTCA	TCTCTGTGA	TGTGAGGCAG	CGCACCATCA	CCTATTTGA	1260
268	CTCGCAGCGT	ACCCCTAAC	GCCGCTGCC	TAAGCATATT	GCCAAGTATC	TACAGGCAGA	1320
269	GGCGTAAAG	AAAGACCGAC	TGGATTTCA	CCAGGGCTGG	AAAGGTTACT	TCAAAATGAA	1380
270	TGTGGCCAGG	CAGAATAATG	ACAGTGACTG	TGGTGTCTTT	GTGTTGCACT	ACTGCAAGCA	1440
271	TCTGGCCCTG	TCTCAGCCAT	TCAGCTTCAC	CCAGCAGGAC	ATGCCAAAC	TTCGTCGGCA	1500
272	GATCTACAAG	GAGCTGTGTC	ACTGCAAATC	CACTGTGTGA	GCCTCGTACC	CCAGACCCCCA	1560
273	AGCCCATAAA	TGGGAAGGG	GACATGGGAG	TCCCTCCCA	AGAAACTCCA	GTCCTTTCC	1620
274	TCTCTGCCT	CTTCCCACTC	ACTTCCCTT	GGTTTTCTAT	ATTTAAATGT	TTCAATTCT	1680
275	GTATTTTTT	TTCTTGAGA	GAATACTGT	TGATTTCTGA	TGTGCAGGGG	GTGGCTACAG	1740
276	AAAAGCCCT	TTCTCCTCT	GTTTGCAGGG	GAGTGTGGCC	CTGTGGCCTG	GGTGGAGCAG	1800

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]